

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Davis, Roger J.
Raingeaud, Joel
Gupta, Shashi
Derijard, Benoit

(ii) TITLE OF INVENTION: CYTOKINE-, STRESS-, AND ONCOPROTEIN-
ACTIVATED HUMAN PROTEIN KINASE KINASES

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fish & Richardson P.C.
(B) STREET: 225 Franklin Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: USA
(F) ZIP: 02110

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPerfect 5.1

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/446,083
(B) FILING DATE: 05/19/95

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Fasse, J. Peter
(B) REGISTRATION NUMBER: 32,983
(C) REFERENCE/DOCKET NUMBER: 04020/09001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 542-5070
(B) TELEFAX: (617) 542-8906

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2030 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

TGGCTGGCAA TGGCCTTGCT GACCTCGAGC CGGGCCCACG TGGGGACCTT TGGAGCACAG 60
CCTACGATCC TGGTGCAAGG CCGGTGGATG CAGAGGCCAG TCCATATACC ACCCAGGCCT 120
GCGAGGAGCG TGGTCCCCAC CCATCCAGCC CATATGTGCA AGTGCCCTTG ACAGAGAGGC 180
TGGTCATATC CATGGTGACC ATTTATGGGC CACAACAGGT CCCCATCTGC GCAGTGAACC 240
CTGTGCTGAG CACCTTGACG ACGTGATCTT GCTTCGTCCT GCAGCACTGT GCGGGGCAGG 300
AAAATCCAAG AGGAAGAAGG ATCTACGGAT ATCCTGCATG TCCAAGCCAC CCGCACCCAA 360
CCCCACACCC CCCCAGAAC TGGACTCCCG GACCTTCATC ACCATTGGAG ACAGAAACTT 420
TGAGGTGGAG GCTGATGACT TGGTGACCAT CTCAGAACTG GGCCGTGGAG CCTATGGGGT 480
GGTAGAGAAG GTGCGGCACG CCCAGAGCGG CACCATCATG GCCGTGAAGC GGATCCGGGC 540
CACCCTGAAC TCACAGGAGC AGAAGCGGCT GCTCATGGAC CTGGACATCA ACATGCGCAC 600
GGTCGACTGT TTCTACACTG TCACCTTCTA CGGGGCACCTA TTCAGAGAGG GAGACGTGTG 660
GATCTGCATG GAGCTCATGG ACACATCCTT GGACAAGTTC TACCGGAAGG TGCTGGATAA 720
AAACATGACA ATTCCAGAGG ACATCCTTGG GGAGATTGCT GTGTCTATCG TGCGGGCCCT 780
GGAGCATCTG CACAGCAAGC TGTGCGTGAT CCACAGAGAT GTGAAGCCCT CCAATGTCTT 840
TATCAACAAG GAGGGCCATG TGAAGATGTG TGACTTTGGC ATCAGTGGCT ACTTGGTGGG 900
CTCTGTGGCC AAGACGATGG ATGCCGGCTG CAAGCCCTAC ATGGCCCTTG AGAGATCAA 960
CCCAGAGCTG AACCAGAAGG GCTACAATGT CAAGTCCGAC GTCTGGAGCC TGGGCATCAC 1020
CATGATTGAG ATGGCCATCC TGCGGTTCCTT TTACGAGTCC TGGGGGACCC CGTTCCAGCA 1080
GCTGAAGCAG GTGGTGGAGG AGCCGTCCCC CCAGCTCCCA GCCGACCGTT TCTCCCCCGA 1140
GTTTGTGGAC TTCCTGCTC AGTGCTCTGAG GAAGAACCCC GCAGAGCGTA TGAGCTACCT 1200
GGAGCTGATG GAGCACCCCT TCTTCACCTT GCACAAAACC AAGAAGACGG ACATTGCTGC 1260
CTTCGTGAAG AAGATCCTGG GAGAAGACTC ATAGGGGCTG GGCCTCGGAC CCCACTCCGG 1320
CCCTCCAGAG CCCCACAGCC CCATCTGCGG GGGCAGTGCT CACCCACACC ATAAGCTACT 1380
GCCATCCTGG CCCAGGGCAT CTGGGAGGAA CCGAGGGGGC TGCTCCACCC TGGCTCTGTG 1440
GCGAGCCATT TGTCCCAAGT GCCAAAGAAG CAGACCATTG GGGCTCCAG CCAGGCCCTT 1500
GTGCGCCCCA CCACTGCCTC TCCCTGCTGC TCCTAGGACC CGTCTCCAGC TGCTGAGATC 1560
CTGGACTGAG GGGGCCTGGA TGCCCCCTGT GGATGCTGCT GCCCCTGCAC AGCAGGCTGC 1620
CAGTGCCTGG GTGGATGGGC CACCGCCTTG CCCAGCCTGG ATGCCATCCA AGTTGTATAT 1680
TTTTTTAATC TCTCGACTGA ATGGACTTTG CACACTTTGG CCCAGGGTGG CCACACCTCT 1740
ATCCCGGCTT TGGTGCGGGG TACACAAGAG GGGATGAGTT GTGTGAATAC CCAAGACTC 1800
CCATGAGGGA GATGCCATGA GCCGCCCAAG GCCTTCCCCT GGCAGTGGCA AACAGGGCCT 1860
CTGCGGAGCA CACTGGCTCA CCCAGTCCTG CCCGCCACCG TTATCGGTGT CATTACCTT 1920
TCGTGTTTTT TTTAATTTAT CCTCTGTTGA TTTTTTCTT TGCTTTATGG GTTTGGCTTG 1980
TTTTTCTTGC ATGTTTTGGA GCTGATCGCT TCTCCCCAC CCCCTAGGGG 2030

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 363 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Pro | Pro | Ala | Pro | Asn | Pro | Thr | Pro | Pro | Arg | Asn | Leu | Asp |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Ser | Arg | Thr | Phe | Ile | Thr | Ile | Gly | Asp | Arg | Met | Phe | Glu | Val | Glu | Ala |
| | | 35 | | | | 40 | | | | | 45 | | | | |
| Asp | Asp | Leu | Val | Thr | Ile | Ser | Glu | Leu | Gly | Arg | Gly | Ala | Tyr | Gly | Val |
| 50 | | | | | | 55 | | | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Lys | Val | Arg | His | Ala | Gln | Ser | Gly | Thr | Ile | Met | Ala | Val | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Arg | Ile | Arg | Ala | Thr | Val | Asn | Ser | Gln | Glu | Gln | Lys | Arg | Leu | Leu | Met |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Asp | Leu | Asp | Ile | Asn | Met | Arg | Thr | Val | Asp | Cys | Phe | Tyr | Thr | Val | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Tyr | Gly | Ala | Leu | Phe | Arg | Glu | Gly | Asp | Val | Trp | Ile | Cys | Met | Glu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Met | Asp | Thr | Ser | Leu | Asp | Lys | Phe | Tyr | Arg | Lys | Val | Leu | Asp | Lys |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asn | Met | Thr | Ile | Pro | Glu | Asp | Ile | Leu | Gly | Glu | Ile | Ala | Val | Ser | Ile |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Val | Arg | Ala | Leu | Glu | His | Leu | His | Ser | Lys | Leu | Ser | Val | Ile | His | Arg |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Asp | Val | Lys | Pro | Ser | Asn | Val | Leu | Ile | Asn | Lys | Glu | Gly | His | Val | Lys |
| | | | 200 | | | | | 205 | | | | | 210 | | |
| Met | Cys | Asp | Phe | Gly | Ile | Ser | Gly | Tyr | Leu | Val | Asp | Ser | Val | Ala | Lys |
| | | 215 | | | | | 220 | | | | | 225 | | | |
| Thr | Met | Asp | Ala | Gly | Cys | Lys | Pro | Tyr | Met | Ala | Pro | Glu | Arg | Ile | Asn |
| | 230 | | | | | 235 | | | | | 240 | | | | |
| Pro | Glu | Leu | Asn | Gln | Lys | Gly | Tyr | Asn | Val | Lys | Ser | Asp | Val | Trp | Ser |
| 245 | | | | | 250 | | | | | 255 | | | | | 260 |
| Leu | Gly | Ile | Thr | Met | Ile | Glu | Met | Ala | Ile | Leu | Arg | Phe | Pro | Tyr | Glu |
| | | | 265 | | | | | | 270 | | | | | 275 | |
| Ser | Trp | Gly | Thr | Pro | Phe | Gln | Gln | Leu | Lys | Gln | Val | Val | Glu | Glu | Pro |
| | | | 280 | | | | | 285 | | | | | 290 | | |
| Ser | Pro | Gln | Leu | Pro | Ala | Asp | Arg | Phe | Ser | Pro | Glu | Phe | Val | Asp | Phe |
| | | 295 | | | | | 300 | | | | | 305 | | | |
| Thr | Ala | Gln | Cys | Leu | Arg | Lys | Asn | Pro | Ala | Glu | Arg | Met | Ser | Tyr | Leu |
| | 310 | | | | | 315 | | | | | 320 | | | | |
| Glu | Leu | Met | Glu | His | Pro | Phe | Phe | Thr | Leu | His | Lys | Thr | Lys | Lys | Thr |
| 325 | | | | 330 | | | | | | 335 | | | 338 | | |
| Asp | Ile | Ala | Ala | Phe | Val | Lys | Lys | Ile | Leu | Gly | Glu | Asp | Ser | | |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1602 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TAGCTGCAGC | ACAGCCTTCC | CTAACGTTGC | AACTGGGGGA | AAAATCACTT | TCCAGTCTGT | 60 |
| TTTGCAAGGT | GTGCATTTCC | ATCTTGATTG | CCTGAAAGTC | CATCTGCTGC | ATCGGTCAAG | 120 |
| AGAAACTCCA | CTTGCATGAA | GATTGCACGC | CTGCAGCTTG | CATCTTTGTT | GCAAACTAG | 180 |
| CTACAGAAGA | GAAGCAAGGC | AAAGTCTTTT | GTGCTCCCCT | CCCCCATCAA | AGGAAAGGGG | 240 |
| AAAATGTCTC | AGTCGAAAGG | CAAGAAGCGA | AACCCTGGCC | TTAAAATTCC | AAAAGAAGCA | 300 |
| TTTGAACAAC | CTCAGACCAG | TTCCACACCA | CCTAGAGATT | TAGACTCCAA | GGCTTGCAAT | 360 |
| TCTATTGGAA | ATCAGAACTT | TGAGGTGAAG | GCAGATGACC | TGGAGCCTAT | AATGGAAGTG | 420 |

```

GGACGAGGTG CGTACGGGGT GGTGGAGAAG ATGCGGCACG TGCCCAGCGG GCAGATCATG 480
GCAGTGAAGC GGATCCGAGC CACAGTAAAT AGCCAGGAAC AGAAACGGCT ACTGATGGAT 540
TTGGATATTT CCATGAGGAC GGTGGACTGT CCATTCACTG TCACCTTTTA TGGCGCACTG 600
TTTCGGGAGG GTGATGTGTG GATCTGCATG GAGCTCATGG ATACATCACT AGATAAATTC 660
TACAAACAAG TTATTGATAA AGGCCAGACA ATTCCAGAGG ACATCTTAGG GAAAATAGCA 720
GTTTCTATTG TAAAAGCATT AGAACATTTA CATAGTAAGC TGTCTGTCAT TCACAGAGAC 780
GTCAAGCCTT CTAATGTACT CATCAATGCT CTCGGTCAAG TGAAGATGTG CGATTTTGGG 840
ATCAGTGGCT ACTTGGTGGA CTCTGTTGCT AAAACAATTG ATGCAGGTTG CAAACCATAC 900
ATGGCCCCTG AAAGAATAAA CCCAGAGCTC AACCAGAAGG GATACAGTGT GAAGTCTGAC 960
ATTTGGAGTC TGGGCATCAC GATGATTGAG TTGGCCATCC TTCGATTTCC CTATGATTCA 1020
TGGGGAACCTC CATTTTCAGCA GCTCAAACAG GTGGTAGAGG AGCCATCGCC ACAACTCCCA 1080
GCAGACAAGT TCTCTGCAGA GTTTGTTGAC TTTACCTCAC AGTGCTTAAA GAAGAATTCC 1140
AAAGAACGGC CTACATACCC AGAGCTAATG CAACATCCAT TTTTCACCCT ACATGAATCC 1200
AAAGGAACAG ATGTGGCATC TTTTGTAATA CTGATTCTTG GAGACTAAAA AGCAGTGGAC 1260
TTAATCGGTT GACCCCTACTG TGGATTGGTG GGTTCGGGG TGAAGCAAGT TCACTACAGC 1320
ATCAATAGAA AGTCATCTTT GAGATAATTT AACCTGCCT CTCAGAGGGT TTTCTCTCCC 1380
AATTTTCTTT TTAATCGGTT GAGATAATTT AACCTGCCT CTCAGAGGGT TTTCTCTCCC 1380
TCTAGATGGA TGAATTATGA TAAAGGCTTA GGACTTCAAA AGGTGATTAA ATATTTAATG 1500
ATGTGTCATA TGAGTCCTCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1560
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA 1602

```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

          5          10          15
Met Ser Gln Ser Lys Gly Lys Lys Arg Asn Pro Gly Leu Lys Ile Pro
          20          25          30
Lys Glu Ala Phe Glu Gln Pro Gln Thr Ser Ser Thr Pro Pro Arg Asp
          35          40          45
Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val
          50          55          60
Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr
          65          70          75          80
Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala
          85          90          95
Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu
          100          105          110
Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe Thr
          115          120          125
Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys
          130          135          140
Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile
          145          150          155          160
Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val

```

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Val | Lys | Ala | Leu | Glu | His | Leu | His | Ser | Lys | Leu | Ser | Val | Ile |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| His | Arg | Asp | Val | Lys | Pro | Ser | Asn | Val | Leu | Ile | Asn | Ala | Leu | Gly | Gln |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Val | Lys | Met | Cys | Asp | Phe | Gly | Ile | Ser | Gly | Tyr | Leu | Val | Asp | Ser | Val |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ala | Lys | Thr | Ile | Asp | Ala | Gly | Cys | Lys | Pro | Tyr | Met | Ala | Pro | Glu | Arg |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ile | Asn | Pro | Glu | Leu | Asn | Gln | Lys | Gly | Tyr | Ser | Val | Lys | Ser | Asp | Ile |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Trp | Ser | Leu | Gly | Ile | Thr | Met | Ile | Glu | Leu | Ala | Ile | Leu | Arg | Phe | Pro |
| | | 260 | | | | | | 265 | | | | | 270 | | |
| Tyr | Asp | Ser | Trp | Gly | Thr | Pro | Phe | Gln | Gln | Leu | Lys | Gln | Val | Val | Glu |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Glu | Pro | Ser | Pro | Gln | Leu | Pro | Ala | Asp | Lys | Phe | Ser | Ala | Glu | Phe | Val |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Asp | Phe | Thr | Ser | Gln | Cys | Leu | Lys | Lys | Asn | Ser | Lys | Glu | Arg | Pro | Thr |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Tyr | Pro | Glu | Leu | Met | Gln | His | Pro | Phe | Phe | Thr | Leu | His | Glu | Ser | Lys |
| | | | | 325 | | | | 330 | | | | | 334 | | |
| Gly | Thr | Asp | Val | Ala | Ser | Phe | Val | Lys | Leu | Ile | Leu | Gly | Asp | | |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| CTAGGGTCCC | CGGCGCCAGG | CCACCCGGCC | GTCAGCAGCA | TGCAGGGTAA | ACGCAAAGCA | 60 |
| CTGAAGTTGA | ATTTTGCAAA | TCCACCTTTC | AAATCTACAG | CAAGGTTTAC | TCTGAATCCC | 120 |
| AATCCTACAG | GAGTTCAAAA | CCCACACATA | GAGAGACTGA | GAACACACAG | CATTGAGTCA | 180 |
| TCAGGAAAAC | TGAAGATCTC | CCCTGAACAA | CACTGGGATT | TCACTGCAGA | GGACTTGAAA | 240 |
| GACCTTGGAG | AAATTGGACG | AGGAGCTTAT | GGTTCTGTCA | ACAAAATGGT | CCACAAACCA | 300 |
| AGTGGGCAAA | TAATGGCAGT | TAAAAGAATT | CGGTCAACAG | TGGATGAAAA | AGAACAAAAA | 360 |
| CAACTTCTTA | TGGATTTGGA | TGTAGTAATG | CGGAGTAGTG | ATTGCCCAT | CATTGTTTCAG | 420 |
| TTTTATGGTG | CACTCTTCAG | AGAGGGTGAC | TGTTGGATCT | GTATGGAAC | CATGTCTACC | 480 |
| TCGTTTGATA | AGTTTACAA | ATATGTATAT | AGTGTATTAG | ATGATGTTAT | TCCAGAAGAA | 540 |
| ATTTTAGGCA | AAATCACTTT | AGCAACTGTG | AAAGCACTAA | ACCACTTAAA | AGAAAACCTTG | 600 |
| AAAATTATTC | ACAGAGATAT | CAAACCTTCC | AATATTCTTC | TGGACAGAAG | TGGAAATATT | 660 |
| AAGCTCTGTG | ACTTCGGCAT | CAGTGGACAG | CTTGTGGACT | CTATTGCCAA | GACAAGAGAT | 720 |
| GCTGGCTGTA | GGCCATACAT | GGCACCTGAA | AGAATAGACC | CAAGCGCATC | ACGACAAGGA | 780 |
| TATGATGTCC | GCTCTGATGT | CTGGAGTTTG | GGGATCACAT | TGTATGAGTT | GGCCACAGGC | 840 |
| CGATTTCTTT | ATCCAAAGTG | GAATAGTGTA | TTTGATCAAC | TAACACAAGT | CGTGAAAGGA | 900 |
| GATCCTCCGC | AGCTGAGTAA | TTCTGAGGAA | AGGGAATTCT | CCCCGAGTTT | CATCAACTTT | 960 |
| GTCAACTTGT | GCCTTACGAA | GGATGAATCC | AAAAGGCCAA | AGTATAAAGA | GCTTCTGAAA | 1020 |
| CATCCCTTTA | TTTTGATGTA | TGAAGAACGT | GCCGTTGAGG | TCGCATGCTA | TGTTTGTAAA | 1080 |

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| ATCCTGGATC | AAATGCCAGC | TACTCCCAGC | TCTCCCATGT | ATGTCGATTG | ATATCGYTGC | 1140 |
| TACATCAGAC | TCTAGAAAAA | AGGGCTGAGA | GGAAGCAAGA | CGTAAAGAAT | TTTCATCCCG | 1200 |
| TATCACAGTG | TTTTTATTGC | TCGCCCAGAC | ACCATGTGCA | ATAAGATTGG | TGTTTCGTTTC | 1260 |
| CATCATGTCT | GTATACTCCT | GTCACCTAGA | ACGTGCATCC | TTGTAATACC | TGATTGATCA | 1320 |
| CACAGTGTTA | GTGCTGGTCA | GAGAGACCTC | ATCCTGCTCT | TTTGTGATGA | ACATATTCAT | 1380 |
| GAAATGTGGA | AGTCAGTACG | ATCAAGTTGT | TGACTGTGAT | TAGATCACAT | CTTAAATTCA | 1440 |
| TTTCTAGACT | CAAAACCTGG | AGATGCAGCT | ACTGGAATGG | TGTTTTGTCA | GACTTCCAAA | 1500 |
| TCCTGGAAGG | ACACAGTGAT | GAATGTACTA | TATCTGAACA | TAGAAACTCG | GGCTTGAGTG | 1560 |
| AGAAGAGCTT | GCACAGCCAA | CGAGACACAT | TGCCTTCTGG | AGCTGGGAGA | CAAAGGAGGA | 1620 |
| ATTTACTTTT | TTCACCAAGT | GCAATAGATT | ACTGATGTGA | TATTCTGTTG | CTTTACAGTT | 1680 |
| ACAGTTGATG | TTTGGGGATC | GATGTGCTCA | GCCAAATTTT | CTGTTTGAAA | TATCATGTTA | 1740 |
| AATTAGAATG | AATTTATCTT | TACCAAAAAC | CATGTTGCGT | TCAAAGAGGT | GAACATTAAA | 1800 |
| ATATAGAGAC | AGGACAGAAT | GTGTTCTTTT | CTCCTCTACC | AGTCCTATTT | TTCAATGGGA | 1860 |
| AGACTCAGGA | GTCTGCCACT | TGTCAAAGAA | GGTGCTGATC | CTAAGAATTT | TTCATTCTCA | 1920 |
| GAATTCGGTG | TGCTGCCAAC | TTGATGTTCC | ACCTGCCACA | AACCACCAGG | ACTGAAAGAA | 1980 |
| GAAAACAGTA | CAGAAGGCAA | AGTTTACAGA | TGTTTTTAAT | TCTAGTATTT | TATCTGGAAC | 2040 |
| AACTTGTAGC | AGCTATATAT | TTCCCCTTGG | TCCCAAGCCT | GATACTTTAG | CCATCATAAC | 2100 |
| TACTAACAG | GGAGAAGTAG | CTAGTAGCAA | TGTGCCTTGA | TTGATTAGAT | AAAGATTTCT | 2160 |
| AGTAGGCAGC | AAAAGACCAA | ATCTCAGTTG | TTTGCTTCTT | GCCATCACTG | GTCCAGGTCT | 2220 |
| TCAGTTTCCG | AATCTCTTTC | CCTTCCCCTG | TGGTCTATTG | TCGCTATGTG | ACTTGCGCTT | 2280 |
| AATCCAATAT | TTTGCCTTTT | TTCTATATCA | AAAAACCTTT | ACAGTTAGCA | GGGATGTTCC | 2340 |
| TTACCGAGGA | TTTTTAAACC | CCAATCTCTC | ATAATCGCTA | GTGTTTAAAA | GGCTAAGAAT | 2400 |
| AGTGGGGCCC | AACCGATGTG | GTAGGTGATA | AAGAGGCATC | TTTTCTAGAG | ACACATTGGA | 2460 |
| CCAGATGAGG | ATCCGAAACG | GCAGCCTTTA | CGTTCATCAC | CTGCTAGAAC | CTCTCGTAGT | 2520 |
| CCATCACCAT | TTCTTGGCAT | TGGAATTCTA | CTGGAAAAAA | ATACAAAAAG | CAAAACAAAA | 2580 |
| CCCTCAGCAC | TGTTACAAGA | GGCCATTTAA | GTATCTTGTT | CTTCTTCACT | TACCCATTAG | 2640 |
| CCAGGTTCTC | ATTAGGTTTT | GCTTGGGCCT | CCCTGGCACT | GAACCTTAGG | CTTTGTATGA | 2700 |
| CAGTGAAGCA | GCACTGTGAG | TGGTTCAAGC | ACACTGGAAT | ATAAAACAGT | CATGGCCTGA | 2760 |
| GATGCAGGTG | ATGCCATTAC | AGAACCAAAT | CGTGGCACGT | ATTGCTGTGT | CTCCTCTCAG | 2820 |
| AGTGACAGTC | ATAAATACTG | TCAAACAATA | AAGGGAGAAT | GGTGCTGTTT | AAAGTCACAT | 2880 |
| CCCTGTAAAT | TGCAGAATTC | AAAAGTGATT | ATCTCTTTGA | TCTACTTGCC | TCATTTCCCT | 2940 |
| ATCTTCTCCC | CCACGGTATC | CTAAACTTTA | GACTTCCCAC | TGTTCTGAAA | GGAGACATTG | 3000 |
| CTCTATGTCT | GCCTTCGACC | ACAGCAAGCC | ATCATCCTCC | ATTGCTCCCC | GGGACTCAAG | 3060 |
| AGGAATCTGT | TTCTCTGCTG | TCAACTTCCC | ATCTGGCTCA | GCATAGGGTC | ACTTTGCCAT | 3120 |
| TATGCAAATG | GAGATAAAAG | CAATTCTGGC | TGTCCAGGAG | CTAATCTGAC | CGTTCTATTG | 3180 |
| TGTGGATGAC | CACATAAGAA | GGCAATTTTA | GTGTATTAAT | CATAGATTAT | TATAAACTAT | 3240 |
| AAACTTAAGG | GCAAGGAGTT | TATTACAATG | TATCTTTATT | AAAACAAAAG | GGTGTATAGT | 3300 |
| GTTCACAAAC | TGTGAAAATA | GTGTAAGAAC | TGTACATTGT | GAGCTCTGGT | TATTTTCTC | 3360 |
| TTGTACCATA | GAAAAATGTA | TAAAAATTAT | CAAAAAGCTA | ATGTGCAGGG | ATATTGCCTT | 3420 |
| ATTTGTCTGT | AAAAAATGGA | GCTCAGTAAC | ATAACTGCTT | CTTGAGCTT | TGGAATATTT | 3480 |
| TATCCTGTAT | TCTTGTTT | | | | | 3498 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | | | 5 | | | | | 10 | | | | | 15 | | |
| Met | Gln | Gly | Lys | Arg | Lys | Ala | Leu | Lys | Leu | Asn | Phe | Ala | Asn | Pro | Pro | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Phe | Lys | Ser | Thr | Ala | Arg | Phe | Thr | Leu | Asn | Pro | Asn | Pro | Thr | Gly | Val | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Gln | Asn | Pro | His | Ile | Glu | Arg | Leu | Arg | Thr | His | Ser | Ile | Glu | Ser | Ser | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Gly | Lys | Leu | Lys | Ile | Ser | Pro | Glu | Gln | His | Trp | Asp | Phe | Thr | Ala | Glu | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Asp | Leu | Lys | Asp | Leu | Gly | Glu | Ile | Gly | Arg | Gly | Ala | Tyr | Gly | Ser | Val | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |
| Asn | Lys | Met | Val | His | Lys | Pro | Ser | Gly | Gln | Ile | Met | Ala | Val | Lys | Arg | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Ile | Arg | Ser | Thr | Val | Asp | Glu | Lys | Glu | Gln | Lys | Gln | Leu | Leu | Met | Asp | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Leu | Asp | Val | Val | Met | Arg | Ser | Ser | Asp | Cys | Pro | Tyr | Ile | Val | Gln | Phe | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Tyr | Gly | Ala | Leu | Phe | Arg | Glu | Gly | Asp | Cys | Trp | Ile | Cys | Met | Glu | Leu | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Met | Ser | Thr | Ser | Phe | Asp | Lys | Phe | Tyr | Lys | Tyr | Val | Tyr | Ser | Val | Leu | |
| | | | | 165 | | | | 170 | | | | | | 175 | | |
| Asp | Asp | Val | Ile | Pro | Glu | Glu | Ile | Leu | Gly | Lys | Ile | Thr | Leu | Ala | Thr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Val | Lys | Ala | Leu | Asn | His | Leu | Lys | Glu | Asn | Leu | Lys | Ile | Ile | His | Arg | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Asp | Ile | Lys | Pro | Ser | Asn | Ile | Leu | Leu | Asp | Arg | Ser | Gly | Asn | Ile | Lys | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Leu | Cys | Asp | Phe | Gly | Ile | Ser | Gly | Gln | Leu | Val | Asp | Ser | Ile | Ala | Lys | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Thr | Arg | Asp | Ala | Gly | Cys | Arg | Pro | Tyr | Met | Ala | Pro | Glu | Arg | Ile | Asp | |
| | | | 245 | | | | | 250 | | | | | | 255 | | |
| Pro | Ser | Ala | Ser | Arg | Gln | Gly | Tyr | Asp | Val | Arg | Ser | Asp | Val | Trp | Ser | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Leu | Gly | Ile | Thr | Leu | Tyr | Glu | Leu | Ala | Thr | Gly | Arg | Phe | Pro | Tyr | Pro | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Lys | Trp | Asn | Ser | Val | Phe | Asp | Gln | Leu | Thr | Gln | Val | Val | Lys | Gly | Asp | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Pro | Pro | Gln | Leu | Ser | Asn | Ser | Glu | Glu | Arg | Glu | Phe | Ser | Pro | Ser | Phe | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Ile | Asn | Phe | Val | Asn | Leu | Cys | Leu | Thr | Lys | Asp | Glu | Ser | Lys | Arg | Pro | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Lys | Tyr | Lys | Glu | Leu | Leu | Lys | His | Pro | Phe | Ile | Leu | Met | Tyr | Glu | Glu | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Arg | Ala | Val | Glu | Val | Ala | Cys | Tyr | Val | Cys | Lys | Ile | Leu | Asp | Gln | Met | |
| | | 355 | | | | | 360 | | | 363 | | | | | | |
| Pro | Ala | Thr | Pro | Ser | Ser | Pro | Met | Tyr | Val | Asp | | | | | | |

(2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3554 base pairs
 (B) TYPE: nucléic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | |
|-------------|------------|------------|------------|-------------|-------------|------|
| CAACAATGGC | GGCTCCGAGC | CCGAGCGGTG | GCGGCGGCAG | CGGCACCCCC | GGCCCCGTAG | 60 |
| GGTCCCCGGC | GCCAGGCCAC | CCGGCCGTCA | GCAGCATGCA | GGGTAAACGC | AAAGCACTGA | 120 |
| AGTTGAATTT | TGCAAATCCA | CCTTTCAAAT | CTACAGCAAG | GTTTACTCTG | AATCCCAATC | 180 |
| CTACAGGAGT | TCAAAACCCA | CACATAGAGA | GACTGAGAAC | ACACAGCATT | GAGTCATCAG | 240 |
| GAAAACTGAA | GATCTCCCCT | GAACAACACT | GGGATTTTAC | TGCAGAGGAC | TTGAAAGACC | 300 |
| TTGGAGAAAT | TGGACGAGGA | GCTTATGGTT | CTGTCAACAA | AATGGTCCAC | AAACCAAGTG | 360 |
| GGCAAATAAT | GGCAGTTAAA | AGAATTCGGT | CAACAGTGGA | TGAAAAAGAA | CAAAAACAAC | 420 |
| TTCTTATGGA | TTTGGATGTA | GTAATGCGGA | GTAGTGATTG | CCCATACATT | GTTTCAGTTT | 480 |
| ATGGTGCACT | CTTCAGAGAG | GGTGACTGTT | GGATCTGTAT | GGAACTCATG | TCTACCTCGT | 540 |
| TTGATAAGTT | TTACAAATAT | GTATATAGTG | TATTAGATGA | TGTTATTCCA | GAAGAAATTT | 600 |
| TAGGCAAAAT | CACTTTAGCA | ACTGTGAAAG | CACTAAACCA | CTTAAAGAA | AACTTGAAAA | 660 |
| TTATTCACAG | AGATATCAAA | CCTTCCAATA | TTCTTCTGGA | CAGAAGTGGA | AATATTAAGC | 720 |
| TCTGTGACTT | CGGCATCAGT | GGACAGCTTG | TGGACTCTAT | TGCCAAGACA | AGAGATGCTG | 780 |
| GCTGTAGGCC | ATACATGGCA | CCTGAAAGAA | TAGACCCAAG | CGCATCACGA | CAAGGATATG | 840 |
| ATGTCCGCTC | TGATGTCTGG | AGTTTGGGGA | TCACATTGTA | TGAGTTGGCC | ACAGGCCGAT | 900 |
| TTCTTATATC | AAAGTGGAAT | AGTGTATTTG | ATCAACTAAC | ACAAGTCGTG | AAAGGAGATC | 960 |
| CTCCGCAGCT | GAGTAATTCT | GAGGAAAGGG | AATTCTCCCC | GAGTTTCATC | AACTTTGTCA | 1020 |
| ACTTGTGCCT | TACGAAGGAT | GAATCCAAAA | GGCCAAAGTA | TAAAGAGCTT | CTGAAACATC | 1080 |
| GCTTTATTTT | GATGTATGAA | GAACGTGCCG | TTGAGGTCGC | ATGCTATGTT | TGTAAAATCC | 1140 |
| TGGATCAAAAT | GCCAGCTACT | CCCAGCTCTC | CCATGTATGT | CGATTGATAT | CGYTGCTACA | 1200 |
| TCAGACTCTA | GAAAAAAGGG | CTGAGAGGAA | GCAAGACGTA | AAGAATTTTC | ATCCCGTATC | 1260 |
| ACAGTGTTTT | TATTGCTCGC | CCAGACACCA | TGTGCAATAA | GATTGGTGTT | CGTTTCCATC | 1320 |
| ATGTCTGTAT | ACTCCTGTCA | CCTAGAACGT | GCATCCTTGT | AATACCTGAT | TGATCACACA | 1380 |
| GTGTTAGTGC | TGGTCAGAGA | GACCTCATCC | TGCTCTTTTG | TGATGAACAT | ATTCATGAAA | 1440 |
| TGTGGAAGTC | AGTACGATCA | AGTTGTTGAC | TGTGATTAGA | TCACATCTTA | AATTCATTTT | 1500 |
| TAGACTCAAA | ACCTGGAGAT | GCAGCTACTG | GAATGGTGTT | TTGTCAGACT | TCCAAATCCT | 1560 |
| GGAAGGACAC | AGTGATGAAT | GTACTATATC | TGAACATAGA | AACTCGGGCT | TGAGTGAGAA | 1620 |
| GAGCTTGCAC | AGCCAACGAG | ACACATTGCC | TTCTGGAGCT | GGGAGACAAA | GGAGGAATTT | 1680 |
| ACTTTCCTCA | CCAAGTGCAA | TAGATTACTG | ATGTGATATT | CTGTTGCTTT | ACAGTTACAG | 1740 |
| TTGATGTTTG | GGGATCGATG | TGCTCAGCCA | AATTTCTGTG | TTGAAATATC | ATGTTAAATT | 1800 |
| AGAATGAATT | TATCTTTACC | AAAAACCATG | TTGCGTTCAA | AGAGGTGAAC | ATTAAAATAT | 1860 |
| AGAGACAGGA | CAGAATGTGT | TCTTTTCTCC | TCTACCAGTC | CTATTTTTC | ATGGGAAGAC | 1920 |
| TCAGGAGTCT | GCCACTTGTC | AAAGAAGGTG | CTGATCCTAA | GAATTTTTC | TTCTCAGAAT | 1980 |
| TCGGTGTGCT | GCCAACCTGA | TGTTCCACCT | GCCACAAACC | ACCAGGACTG | AAAGAAGAAA | 2040 |
| ACAGTACAGA | AGGCAAAGTT | TACAGATGTT | TTTAATTCTA | GTATTTTATC | TGGAACAAC | 2100 |
| TGTAGCAGCT | ATATATTTCC | CCTTGGTCCC | AAGCCTGATA | CTTTAGCCAT | CATAACTCAC | 2160 |
| TAACAGGGAG | AAGTAGCTAG | TAGCAATGTG | CCTTGATTGA | TTAGATAAAG | ATTTCTAGTA | 2220 |
| GGCAGCAAAA | GACCAAATCT | CAGTTGTTTG | CTTCTTGCCA | TCACTGGTCC | AGGTCTTCAG | 2280 |
| TTTCCGAATC | TCTTTCCCTT | CCCCTGTGGT | CTATTGTGCG | TATGTGACTT | GCGCTTAATC | 2340 |
| CAATATTTTG | CCTTTTTTCT | ATATCAAAAA | ACCTTTACAG | TTAGCAGGGA | TGTTCCCTTAC | 2400 |
| CGAGGATTTT | TAACCCCCAA | TCTCTCATAA | TCGCTAGTGT | TTAAAAGGCT | AAGAATAGTG | 2460 |
| GGGCCCAACC | GATGTGGTAG | GTGATAAAGA | GGCATCTTTT | CTAGAGACAC | ATTGGACCAG | 2520 |
| ATGAGGATCC | GAAACGGCAG | CCTTTACGTT | CATCACCTGC | TAGAACCCTCT | CGTAGTCCAT | 2580 |


```

CACCATTCTTCT TGGCATTGGA ATTCTACTGG AAAAAAATAC AAAAAAGCAAA AAAAAACCCT 2640
CAGCACTGTT ACAAGAGGCC ATTTAAGTAT CTTGTGCTTC TTCACCTACC CATTAGCCAG 2700
GTTCTCATTA GGTTTTGCTT GGGCCTCCCT GGCAGTGAAC CTTAGGCTTT GTATGACAGT 2760
GAAGCAGCAC TGTGAGTGGT TCAAGCACAC TGGAATATAA AACAGTCATG GCCTGAGATG 2820
CAGGTGATGC CATTACAGAA CCAAATCGTG GCACGTATTG CTGTGTCTCC TCTCAGAGTG 2880
ACAGTCATAA ATACTGTCAA ACAATAAAGG GAGAATGGTG CTGTTTAAAG TCACATCCCT 2940
GTAAATTGCA GAATTCAAAA GTGATTATCT CTTTGATCTA CTTGCCTCAT TTCCCTATCT 3000
TCTCCCCCAC GGTATCCTAA ACTTTAGACT TCCCCTGTT CTGAAAGGAG ACATTGCTCT 3060
ATGTCTGCCT TCGACCACAG CAAGCCATCA TCCTCCATTG CTCCCGGGGA CTCAAGAGGA 3120
ATCTGTTTCT CTGCTGTCAA CTTCCCCTCT GGCTCAGCAT AGGGTCACTT TGCCATTATG 3180
CAAATGGAGA TAAAAGCAAT TCTGGCTGTC CAGGAGCTAA TCTGACCGTT CTATTGTGTG 3240
GATGACCACA TAAGAAGGCA ATTTTAGTGT ATTAATCATA GATTATTATA AACTATAAAC 3300
TTAAGGGCAA GGAGTTTATT ACAATGTATC TTTATTAAAA CAAAAGGGTG TATAGTGTTC 3360
ACAACTGTG AAAATAGTGT AAGAACTGTA CATTGTGAGC TCTGGTTATT TTTCTCTTGT 3420
ACCATAGAAA AATGTATAAA AATTATCAAA AAGCTAATGT GCAGGGATAT TGCCTTATTT 3480
GTCTGTAAAA AATGGAGCTC AGTAACATAA CTGCTTCTTG GAGCTTTGGA ATATTTTATC 3540
CTGTATTCTT GTTT

```

3554

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Pro | Ser | Pro | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Thr | Pro | Gly |
| | | | 20 | | | | 25 | | | | 30 | | | | |
| Pro | Val | Gly | Ser | Pro | Ala | Pro | Gly | His | Pro | Ala | Val | Ser | Ser | Met | Gln |
| | | 35 | | | | | 40 | | | | 45 | | | | |
| Gly | Lys | Arg | Lys | Ala | Leu | Lys | Leu | Asn | Phe | Ala | Asn | Pro | Pro | Phe | Lys |
| | | 50 | | | | 55 | | | | 60 | | | | | |
| Ser | Thr | Ala | Arg | Phe | Thr | Leu | Asn | Pro | Asn | Pro | Thr | Gly | Val | Gln | Asn |
| | | 65 | | | 70 | | | | 75 | | | | | 80 | |
| Pro | His | Ile | Glu | Arg | Leu | Arg | Thr | His | Ser | Ile | Glu | Ser | Ser | Gly | Lys |
| | | | 85 | | | | 90 | | | | 95 | | | | |
| Leu | Lys | Ile | Ser | Pro | Glu | Gln | His | Trp | Asp | Phe | Thr | Ala | Glu | Asp | Leu |
| | | | 100 | | | | 105 | | | | 110 | | | | |
| Lys | Asp | Leu | Gly | Glu | Ile | Gly | Arg | Gly | Ala | Tyr | Gly | Ser | Val | Asn | Lys |
| | | 115 | | | | 120 | | | | 125 | | | | | |
| Met | Val | His | Lys | Pro | Ser | Gly | Gln | Ile | Met | Ala | Val | Lys | Arg | Ile | Arg |
| | | 130 | | | | 135 | | | | 140 | | | | | |
| Ser | Thr | Val | Asp | Glu | Lys | Glu | Gln | Lys | Gln | Leu | Leu | Met | Asp | Leu | Asp |
| | | 145 | | | 150 | | | | | 155 | | | | 160 | |
| Val | Val | Met | Arg | Ser | Ser | Asp | Cys | Pro | Tyr | Ile | Val | Gln | Phe | Tyr | Gly |
| | | | 165 | | | | 170 | | | | | | 175 | | |
| Ala | Leu | Phe | Arg | Glu | Gly | Asp | Cys | Trp | Ile | Cys | Met | Glu | Leu | Met | Ser |
| | | | 180 | | | | 185 | | | | | 190 | | | |
| Thr | Ser | Phe | Asp | Lys | Phe | Tyr | Lys | Tyr | Val | Tyr | Ser | Val | Leu | Asp | Asp |

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|------|
| AGCGCATCAC | GACAAGGATA | TGATGTCCGC | TCTGATGTCT | GGAGTTTGGG | GATCACATTG | 900 |
| TATGAGTTGG | CCACAGGCCG | ATTTCCCTTAT | CCAAAGTGGA | ATAGTGTATT | TGATCAACTA | 960 |
| ACACAAGTCG | TGAAAGGAGA | TCCTCCGCAG | CTGAGTAATT | CTGAGGAAAG | GGAATTCTCC | 1020 |
| CCGAGTTTCA | TCAACTTTGT | CAACTTGTGC | CTTACGAAGG | ATGAATCCAA | AAGGCCAAAG | 1080 |
| TATAAAGAGC | TTCTGAAACA | TCCCTTTATT | TTGATGTATG | AAGAACGTGC | CGTTGAGGTC | 1140 |
| GCATGCTATG | TTTGTAAAAT | CCTGGATCAA | ATGCCAGCTA | CTCCCAGCTC | TCCCATGTAT | 1200 |
| GTCGATTGAT | ATCGCTGCTA | CATCAGACTC | TAGAAAAAAG | GGCTGAGAGG | AAGCAAGACG | 1260 |
| TAAAGAATTT | TCATCCCGTA | TCACAGTGTT | TTTATTGCTC | GCCCAGACAC | CATGTGCAAT | 1320 |
| AAGATTGGTG | TTCGTTTCCA | TCATGTCTGT | ATACTCCTGT | CACCTAGAAC | GTGCATCCTT | 1380 |
| GTAATACCTG | ATTGATCACA | CAGTGTTAGT | GCTGGTCAGA | GAGACCTCAT | CCTGCTCTTT | 1440 |
| TGTGATGAAC | ATATTTCATG | AATGTGGAAG | TCAGTACGAT | CAAGTTGTTG | ACTGTGATTA | 1500 |
| GATCACATCT | TAAATTCATT | TCTAGACTCA | AAACCTGGAG | ATGCAGCTAC | TGGAATGGTG | 1560 |
| TTTTGTCAGA | CTTCCAAATC | CTGGAAGGAC | ACAGTGATGA | ATGTACTATA | TCTGAACATA | 1620 |
| GAAACTCGGG | CTTGAGTGAG | AAGAGCTTGC | ACAGCCAACG | AGACACATTG | CCTTCTGGAG | 1680 |
| CTGGGAGACA | AAGGAGGAAT | TTACTTTCTT | CACCAAGTGC | AATAGATTAC | TGATGTGATA | 1740 |
| TTCTGTTGCT | TTACAGTTAC | AGTTGATGTT | TGGGGATCGA | TGTGCTCAGC | CAAATTCCTT | 1800 |
| GTTTGAAATA | TCATGTTAAA | TTAGAATGAA | TTTATCTTTA | CCAAAAACCA | TGTTGCGTTC | 1860 |
| AAAGAGGTGA | ACATTAAAAT | ATAGAGACAG | GACAGAATGT | GTTCTTTTCT | CCTCTACCAG | 1920 |
| TCCTATTTTT | CAATGGGAAG | ACTCAGGAGT | CTGCCACTTG | TCAAAGAAGG | TGCTGATCCT | 1980 |
| AAGAATTTTT | CATTCTCAGA | ATTCGGTGTG | CTGCCAACTT | GATGTTCCAC | CTGCCACAAA | 2040 |
| CCACCAGGAC | TGAAAGAAGA | AAACAGTACA | GAAGGCAAAG | TTTACAGATG | TTTTTAATTC | 2100 |
| TAGTATTTTA | TCTGGAACAA | CTTGTAGCAG | CTATATATTT | CCCCTTGGTC | CCAAGCCTGA | 2160 |
| FACTTTAGCC | ATCATAACTC | ACTAACAGGG | AGAAGTAGCT | AGTAGCAATG | TGCCTTGATT | 2220 |
| GATTAGATAA | AGATTTCTAG | TAGGCAGCAA | AAGACCAAAT | CTCAGTTGTT | TGCTTCTTGC | 2340 |
| CATCACTGGT | CCAGGTCTTC | AGTTTCCGAA | TCTCTTTCCC | TTCCCCTGTG | GTCTATTGTC | 2400 |
| GCTATGTGAC | TTGCGCTTAA | TCCAATATTT | TGCCTTTTTT | CTATATCAAA | AAACCTTTAC | 2460 |
| AGTTAGCAGG | GATGTTCCCT | ACCGAGGATT | TTTAACCCCC | AATCTCTCAT | AATCGCTAGT | 2520 |
| GTTTAAAAGG | CTAAGAATAG | TGGGGCCCAA | CCGATGTGGT | AGGTGATAAA | GAGGCATCTT | 2580 |
| TTCTAGAGAC | ACATTGGACC | AGATGAGGAT | CCGAAACGGC | AGCCTTTACG | TTCATCACCT | 2640 |
| GCTAGAACCT | CTCGTAGTCC | ATCACCATTT | CTTGGCATTG | GAATTCTACT | GGAAAAAAT | 2700 |
| ACAAAAAGCA | AAACAAAACC | CTCAGCACTG | TTACAAGAGG | CCATTTAAGT | ATCTTGTGCT | 2760 |
| TCCTTCACTTA | CCCATTAGCC | AGGTTCTCAT | TAGGTTTTTG | TTGGGCCTCC | CTGGCACTGA | 2820 |
| ACCTTAGGCT | TTGTATGACA | GTGAAGCAGC | ACTGTGAGTG | GTTCAAGCAC | ACTGGAATAT | 2880 |
| AAAACAGTCA | TGGCCTGAGA | TGCAGGTGAT | GCCATTACAG | AACCAAATCG | TGGCACGTAT | 2940 |
| TGCTGTGTCT | CCTCTCAGAG | TGACAGTCAT | AAATACTGTC | AAACAATAAA | GGGAGAATGG | 3000 |
| TGCTGTTTAA | AGTCACATCC | CTGTAAATTG | CAGAATTCAA | AAGTGATTAT | CTCTTTGATC | 3060 |
| TACTTGCCCTC | ATTTCCCTAT | CTTCTCCCCC | ACGGTATCCT | AAACTTTAGA | CTTCCCCTG | 3120 |
| TTCTGAAAGG | AGACATTGCT | CTATGTCTGC | CTTCGACCAC | AGCAAGCCAT | CATCCTCCAT | 3180 |
| TGCTCCCGGG | GACTCAAGAG | GAATCTGTTT | CTCTGCTGTC | AACTTCCCCT | CTGGCTCAGC | 3240 |
| ATAGGGTCAC | TTTGCCATTA | TGCAAATGGA | GATAAAAGCA | ATTCTGGCTG | TCCAGGAGCT | 3300 |
| AATCTGACCG | TTCTATTGTG | TGGATGACCA | CATAAGAAGG | CAATTTTAGT | GTATTAATCA | 3360 |
| TAGATTATTA | TAAACTATAA | ACTTAAGGGC | AAGGAGTTTA | TTACAATGTA | TCTTTATTAA | 3420 |
| AACAAAAGGG | TGTATAGTGT | TCACAACTG | TGAAAATAGT | GTAAGAACTG | TACATTGTGA | 3480 |
| GCTCTGGTTA | TTTTTCTCTT | GTACCATAGA | AAAATGTATA | AAAATTATCA | AAAAGCTAAT | 3540 |
| GTGCAGGGAT | ATTGCCTTAT | TTGTCTGTAA | AAAATGGAGC | TCAGTAACAT | AACTGCTTCT | 3600 |
| TGGAGCTTTG | GAATATTTTA | TCCTGTATTC | TTGTTT | | | 3636 |

(2) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids
 (B) TYPE: peptide
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Pro | Ser | Pro | Ser | Gly | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Ser | Gly | Thr | Pro | Gly | Pro | Val | Gly | Ser | Pro | Ala | Pro | Gly | His | Pro |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Val | Ser | Ser | Met | Gln | Gly | Lys | Arg | Lys | Ala | Leu | Lys | Leu | Asn | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | Asn | Pro | Pro | Phe | Lys | Ser | Thr | Ala | Arg | Phe | Thr | Leu | Asn | Pro | Asn |
| | 65 | | | | 70 | | | | 75 | | | | | | 80 |
| Pro | Thr | Gly | Val | Gln | Asn | Pro | His | Ile | Glu | Arg | Leu | Arg | Thr | His | Ser |
| | | | | 85 | | | | 90 | | | | | 95 | | |
| Ile | Glu | Ser | Ser | Gly | Lys | Leu | Lys | Ile | Ser | Pro | Glu | Gln | His | Trp | Asp |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Phe | Thr | Ala | Glu | Asp | Leu | Lys | Asp | Leu | Gly | Glu | Ile | Gly | Arg | Gly | Ala |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Tyr | Gly | Ser | Val | Asn | Lys | Met | Val | His | Lys | Pro | Ser | Gly | Gln | Ile | Met |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Val | Lys | Arg | Ile | Arg | Ser | Thr | Val | Asp | Glu | Lys | Glu | Gln | Lys | Gln |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 |
| Leu | Leu | Met | Asp | Leu | Asp | Val | Val | Met | Arg | Ser | Ser | Asp | Cys | Pro | Tyr |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Ile | Val | Gln | Phe | Tyr | Gly | Ala | Leu | Phe | Arg | Glu | Gly | Asp | Cys | Trp | Ile |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Cys | Met | Glu | Leu | Met | Ser | Thr | Ser | Phe | Asp | Lys | Phe | Tyr | Lys | Tyr | Val |
| | 195 | | | | | 200 | | | | | | 205 | | | |
| Tyr | Ser | Val | Leu | Asp | Asp | Val | Ile | Pro | Glu | Glu | Ile | Leu | Gly | Lys | Ile |
| | 210 | | | | | 215 | | | | | | 220 | | | |
| Thr | Leu | Ala | Thr | Val | Lys | Ala | Leu | Asn | His | Leu | Lys | Glu | Asn | Leu | Lys |
| | 225 | | | | 230 | | | | | 235 | | | | | 240 |
| Ile | Ile | His | Arg | Asp | Ile | Lys | Pro | Ser | Asn | Ile | Leu | Leu | Asp | Arg | Ser |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Gly | Asn | Ile | Lys | Leu | Cys | Asp | Phe | Gly | Ile | Ser | Gly | Gln | Leu | Val | Asp |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ser | Ile | Ala | Lys | Thr | Arg | Asp | Ala | Gly | Cys | Arg | Pro | Tyr | Met | Ala | Pro |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Glu | Arg | Ile | Asp | Pro | Ser | Ala | Ser | Arg | Gln | Gly | Tyr | Asp | Val | Arg | Ser |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Asp | Val | Trp | Ser | Leu | Gly | Ile | Thr | Leu | Tyr | Glu | Leu | Ala | Thr | Gly | Arg |
| | 305 | | | | 310 | | | | | 315 | | | | | 320 |
| Phe | Pro | Tyr | Pro | Lys | Trp | Asn | Ser | Val | Phe | Asp | Gln | Leu | Thr | Gln | Val |
| | | | 325 | | | | | | 330 | | | | | 335 | |
| Val | Lys | Gly | Asp | Pro | Pro | Gln | Leu | Ser | Asn | Ser | Glu | Glu | Arg | Glu | Phe |
| | | | 340 | | | | 345 | | | | | | 350 | | |
| Ser | Pro | Ser | Phe | Ile | Asn | Phe | Val | Asn | Leu | Cys | Leu | Thr | Lys | Asp | Glu |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| Ser | Lys | Arg | Pro | Lys | Tyr | Lys | Glu | Leu | Leu | Lys | His | Pro | Phe | Ile | Leu | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |
| Met | Tyr | Glu | Glu | Arg | Ala | Val | Glu | Val | Ala | Cys | Tyr | Val | Cys | Lys | Ile | | |
| 385 | | | | | 390 | | | | | 395 | | | | 399 | | | |
| Leu | Asp | Gln | Met | Pro | Ala | Thr | Pro | Ser | Ser | Pro | Met | Tyr | Val | Asp | | | |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Met | Pro | Lys | Lys | Lys | Pro | Thr | Pro | Ile | Gln | Leu | Asn | Pro | Ala | Pro | Asp | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Gly | Ser | Ala | Val | Asn | Gly | Thr | Ser | Ser | Ala | Glu | Thr | Asn | Leu | Glu | Ala | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Leu | Gln | Lys | Lys | Leu | Glu | Glu | Leu | Glu | Leu | Asp | Glu | Gln | Gln | Arg | Lys | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| Arg | Leu | Glu | Ala | Phe | Leu | Thr | Gln | Lys | Gln | Lys | Val | Gly | Glu | Leu | Lys | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| Asp | Asp | Asp | Phe | Glu | Lys | Ile | Ser | Glu | Leu | Gly | Ala | Gly | Asn | Gly | Gly | | |
| | | | 85 | | | | | 90 | | | | | 95 | | | | |
| Val | Val | Phe | Lys | Val | Ser | His | Lys | Pro | Ser | Gly | Leu | Val | Met | Ala | Arg | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Lys | Leu | Ile | His | Leu | Glu | Ile | Lys | Pro | Ala | Ile | Arg | Asn | Gln | Ile | Ile | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Arg | Glu | Leu | Gln | Val | Leu | His | Glu | Cys | Asn | Ser | Pro | Tyr | Ile | Val | Gly | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| Phe | Tyr | Gly | Ala | Phe | Tyr | Ser | Asp | Gly | Glu | Ile | Ser | Ile | Cys | Met | Glu | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| His | Met | Asp | Gly | Gly | Ser | Leu | Asp | Gln | Val | Leu | Lys | Lys | Ala | Gly | Arg | | |
| | | | 165 | | | | | 170 | | | | | | 175 | | | |
| Ile | Pro | Glu | Gln | Ile | Leu | Gly | Lys | Val | Ser | Ile | Ala | Val | Ile | Lys | Gly | | |
| | | 180 | | | | | | 185 | | | | | 190 | | | | |
| Leu | Thr | Tyr | Leu | Arg | Glu | Lys | His | Lys | Ile | Met | His | Arg | Asp | Val | Lys | | |
| | 195 | | | | | | 200 | | | | | 205 | | | | | |
| Pro | Ser | Asn | Ile | Leu | Val | Asn | Ser | Arg | Gly | Glu | Ile | Lys | Leu | Cys | Asp | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| Phe | Gly | Val | Ser | Gly | Gln | Leu | Ile | Asp | Ser | Met | Ala | Asn | Ser | Phe | Val | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Gly | Thr | Arg | Ser | Tyr | Met | Ser | Pro | Glu | Arg | Leu | Gln | Gly | Thr | His | Tyr | | |
| | | | 245 | | | | | 250 | | | | | | 255 | | | |
| Ser | Val | Gln | Ser | Asp | Ile | Trp | Ser | Met | Gly | Leu | Ser | Leu | Val | Glu | Met | | |
| | | 260 | | | | | | 265 | | | | | 270 | | | | |
| Ala | Val | Gly | Arg | Tyr | Pro | Ile | Pro | Pro | Pro | Asp | Ala | Lys | Glu | Leu | Glu | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 275 | | 280 | | 285 | | | | | | | | | | |
| Leu | Met | Phe | Gly | Cys | Gln | Val | Glu | Gly | Asp | Ala | Ala | Glu | Thr | Pro | Pro |
| | 290 | | | | 295 | | | | | 300 | | | | | |
| Arg | Pro | Arg | Thr | Pro | Gly | Arg | Pro | Leu | Ser | Ser | Tyr | Gly | Met | Asp | Ser |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Arg | Pro | Pro | Met | Ala | Ile | Phe | Glu | Leu | Leu | Asp | Tyr | Ile | Val | Asn | Glu |
| | | | | 325 | | | | | | 330 | | | | 335 | |
| Pro | Pro | Pro | Lys | Leu | Pro | Ser | Gly | Val | Phe | Ser | Leu | Glu | Phe | Gln | Asp |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Phe | Val | Asn | Lys | Cys | Leu | Ile | Lys | Asn | Pro | Ala | Glu | Arg | Ala | Asp | Leu |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Lys | Gln | Leu | Met | Val | His | Ala | Phe | Ile | Lys | Arg | Ser | Asp | Ala | Glu | Glu |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Val | Asp | Phe | Ala | Gly | Trp | Leu | Cys | Ser | Thr | Ile | Gly | Leu | Asn | Gln | Pro |
| 385 | | | | | 390 | | | 393 | | | | | | | |
| Ser | Thr | Pro | Thr | His | Ala | Ala | Gly | Val | | | | | | | |

- (2) INFORMATION FOR SEQ ID NO:12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 amino acids
 - (B) TYPE: peptide
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|
| | | 5 | | 10 | | 15 |
| Met | Leu | Ala | Arg | Arg | Lys | Pro |
| | | 20 | | 25 | | 30 |
| Thr | Ile | Ala | Glu | Gly | Pro | Ser |
| | | 35 | | 40 | | 45 |
| Asn | Leu | Val | Asp | Leu | Gln | Lys |
| | | 50 | | 55 | | 60 |
| Gln | Gln | Lys | Lys | Arg | Leu | Glu |
| | | 65 | | 70 | | 75 |
| Ser | Glu | Leu | Lys | Asp | Asp | Phe |
| | | 85 | | 90 | | 95 |
| Gly | Asn | Gly | Gly | Val | Val | Thr |
| | | 100 | | 105 | | 110 |
| Ile | Met | Ala | Arg | Lys | Leu | Ile |
| | | 115 | | 120 | | 125 |
| Asn | Gln | Ile | Ile | Arg | Glu | Leu |
| | | 130 | | 135 | | 140 |
| Tyr | Ile | Val | Gly | Phe | Tyr | Gly |
| | | 145 | | 150 | | 155 |
| Ile | Cys | Met | Glu | His | Met | Asp |
| | | 165 | | 170 | | 175 |
| Glu | Ala | Lys | Arg | Ile | Pro | Glu |
| | | 180 | | 185 | | 190 |
| Val | Leu | Arg | Gly | Leu | Ala | Tyr |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| | 195 | | 200 | | 205 | | | | | | | | | | | | | | |
| Arg | Asp | Val | Lys | Pro | Ser | Asn | Ile | Leu | Val | Asn | Ser | Arg | Gly | Glu | Ile | | | | |
| | 210 | | | | | 215 | | | | 220 | | | | | | | | | |
| Lys | Leu | Cys | Asp | Phe | Gly | Val | Ser | Gly | Gln | Leu | Ile | Asp | Ser | Met | Ala | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | | |
| Asn | Ser | Phe | Val | Gly | Thr | Arg | Ser | Tyr | Met | Ala | Pro | Glu | Arg | Leu | Gln | | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | | |
| Gly | Thr | His | Tyr | Ser | Val | Gln | Ser | Asp | Ile | Trp | Ser | Met | Gly | Leu | Ser | | | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | | | |
| Leu | Val | Glu | Leu | Ala | Val | Gly | Arg | Tyr | Pro | Ile | Pro | Pro | Pro | Asp | Ala | | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | | | |
| Lys | Glu | Leu | Glu | Ala | Ile | Phe | Gly | Arg | Pro | Val | Val | Asp | Gly | Glu | Glu | | | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | | | |
| Gly | Glu | Pro | His | Ser | Ile | Ser | Pro | Arg | Pro | Arg | Pro | Pro | Gly | Arg | Pro | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | | |
| Val | Ser | Gly | His | Gly | Met | Asp | Ser | Arg | Pro | Ala | Met | Ala | Ile | Phe | Glu | | | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | | | |
| Leu | Leu | Asp | Tyr | Ile | Val | Asn | Glu | Pro | Pro | Pro | Lys | Leu | Pro | Asn | Gly | | | | |
| | | | 340 | | | | | 345 | | | | 350 | | | | | | | |
| Val | Phe | Thr | Pro | Asp | Phe | Gln | Glu | Phe | Val | Asn | Lys | Cys | Leu | Ile | Lys | | | | |
| | | 355 | | | | 360 | | | | | 365 | | | | | | | | |
| Asn | Pro | Ala | Glu | Arg | Ala | Asp | Leu | Lys | Met | Leu | Thr | Asn | His | Thr | Phe | | | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | | | |
| Ile | Lys | Arg | Ser | Glu | Val | Glu | Glu | Val | Asp | Phe | Ala | Gly | Trp | Leu | Cys | | | | |
| 385 | | | | | 390 | | | | 395 | | | | | 400 | | | | | |
| Lys | Thr | Leu | Arg | Leu | Asn | Gln | Pro | Gly | Thr | Pro | Thr | Arg | Thr | Ala | Val | | | | |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 amino acids

(B) TYPE: peptide

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| | | | 5 | | | | 10 | | | | | 15 | | | | | | | |
| Met | Glu | Asp | Lys | Phe | Ala | Asn | Leu | Ser | Leu | His | Glu | Lys | Thr | Gly | Lys | | | | |
| | | | 20 | | | | 25 | | | | | 30 | | | | | | | |
| Ser | Ser | Ile | Gln | Leu | Asn | Glu | Gln | Thr | Gly | Ser | Asp | Asn | Gly | Ser | Ala | | | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | | | |
| Val | Lys | Arg | Thr | Ser | Ser | Thr | Ser | Ser | His | Tyr | Asn | Asn | Ile | Asn | Ala | | | | |
| | | | 50 | | | 55 | | | | | 60 | | | | | | | | |
| Asp | Leu | His | Ala | Arg | Val | Lys | Ala | Phe | Gln | Glu | Gln | Arg | Ala | Leu | Lys | | | | |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | | | | | |
| Arg | Ser | Ala | Ser | Val | Gly | Ser | Asn | Gln | Ser | Glu | Gln | Asp | Lys | Gly | Ser | | | | |
| | | | 85 | | | | 90 | | | | | | 95 | | | | | | |
| Ser | Gln | Ser | Pro | Lys | His | Ile | Gln | Gln | Ile | Val | Asn | Lys | Pro | Leu | Pro | | | | |
| | | | 100 | | | | 105 | | | | | 110 | | | | | | | |
| Pro | Leu | Pro | Val | Ala | Gly | Ser | Ser | Lys | Val | Ser | Gln | Arg | Met | Ser | Ser | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Gln | Val | Val | Gln | Ala | Ser | Ser | Lys | Ser | Thr | Leu | Lys | Asn | Val | Leu | Asp | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Asn | Gln | Glu | Thr | Gln | Asn | Ile | Thr | Asp | Val | Asn | Ile | Asn | Ile | Asp | Thr | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Thr | Lys | Ile | Thr | Ala | Thr | Thr | Ile | Gly | Val | Asn | Ile | Gly | Leu | Pro | Ala | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Thr | Asp | Ile | Thr | Pro | Ser | Val | Ser | Asn | Thr | Ala | Ser | Ala | Thr | His | Lys | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Ala | Gln | Leu | Leu | Asn | Pro | Asn | Arg | Arg | Ala | Pro | Arg | Arg | Pro | Leu | Ser | |
| | 195 | | | | | 200 | | | | | | 205 | | | | |
| Thr | Gln | His | Pro | Thr | Arg | Pro | Asn | Val | Ala | Pro | His | Lys | Ala | Pro | Ala | |
| 210 | | | | | | 215 | | | | | 220 | | | | | |
| Ile | Ile | Asn | Thr | Pro | Lys | Gln | Ser | Leu | Ser | Ala | Arg | Arg | Gly | Leu | Lys | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Leu | Pro | Pro | Gly | Gly | Met | Ser | Leu | Lys | Met | Pro | Thr | Lys | Thr | Ala | Gln | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Gln | Pro | Gln | Gln | Phe | Ala | Pro | Ser | Pro | Ser | Asn | Lys | Lys | His | Ile | Glu | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Thr | Leu | Ser | Asn | Ser | Lys | Val | Val | Glu | Gly | Lys | Arg | Ser | Asn | Pro | Gly | |
| | 275 | | | | | 280 | | | | | 285 | | | | | |
| Ser | Leu | Ile | Asn | Gly | Val | Gln | Ser | Thr | Ser | Thr | Ser | Ser | Ser | Thr | Glu | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Gly | Pro | His | Asp | Thr | Val | Gly | Thr | Thr | Pro | Arg | Thr | Gly | Asn | Ser | Asn | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Asn | Ser | Ser | Asn | Ser | Gly | Ser | Ser | Gly | Gly | Gly | Gly | Leu | Phe | Ala | Asn | |
| | | | | 325 | | | | 330 | | | | | 335 | | | |
| Phe | Ser | Lys | Tyr | Val | Asp | Ile | Lys | Ser | Gly | Ser | Leu | Asn | Phe | Ala | Gly | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Lys | Leu | Ser | Leu | Ser | Ser | Lys | Gly | Ile | Asp | Phe | Ser | Asn | Gly | Ser | Ser | |
| | 355 | | | | | 360 | | | | | 365 | | | | | |
| Ser | Arg | Ile | Thr | Leu | Asp | Glu | Leu | Glu | Phe | Leu | Asp | Glu | Leu | Gly | His | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Gly | Asn | Tyr | Gly | Asn | Val | Ser | Lys | Val | Leu | His | Lys | Pro | Thr | Asn | Val | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Ile | Met | Ala | Thr | Lys | Glu | Val | Arg | Leu | Glu | Leu | Asp | Glu | Ala | Lys | Phe | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| Arg | Gln | Ile | Leu | Met | Glu | Leu | Glu | Val | Leu | His | Lys | Cys | Asn | Ser | Pro | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| Tyr | Ile | Val | Asp | Phe | Tyr | Gly | Ala | Phe | Phe | Ile | Glu | Gly | Ala | Val | Tyr | |
| | 435 | | | | | 440 | | | | | 445 | | | | | |
| Met | Cys | Met | Glu | Tyr | Met | Asp | Gly | Gly | Ser | Leu | Asp | Lys | Ile | Tyr | Asp | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| Glu | Ser | Ser | Glu | Ile | Gly | Gly | Ile | Asp | Glu | Pro | Gln | Leu | Ala | Phe | Ile | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Ala | Asn | Ala | Val | Ile | His | Gly | Leu | Lys | Glu | Leu | Lys | Glu | Gln | His | Asn | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| Ile | Ile | His | Arg | Asp | Val | Lys | Pro | Thr | Asn | Ile | Leu | Cys | Ser | Ala | Asn | |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| | | | 500 | | | | | 505 | | | | | 510 | | | | |
| Gln | Gly | Thr | Val | Lys | Leu | Cys | Asp | Phe | Gly | Val | Ser | Gly | Asn | Leu | Val | | |
| | | 515 | | | | | 520 | | | | | 525 | | | | | |
| Ala | Ser | Leu | Ala | Lys | Thr | Asn | Ile | Gly | Cys | Gln | Ser | Tyr | Met | Ala | Pro | | |
| | | 530 | | | | 535 | | | | | 540 | | | | | | |
| Glu | Arg | Ile | Lys | Ser | Leu | Asn | Pro | Asp | Arg | Ala | Thr | Tyr | Thr | Val | Gln | | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | | |
| Ser | Asp | Ile | Trp | Ser | Leu | Gly | Leu | Ser | Ile | Leu | Glu | Met | Ala | Leu | Gly | | |
| | | | 565 | | | | | 570 | | | | | | 575 | | | |
| Arg | Tyr | Pro | Tyr | Pro | Pro | Glu | Thr | Tyr | Asp | Asn | Ile | Phe | Ser | Gln | Leu | | |
| | | 580 | | | | | | 585 | | | | | | 590 | | | |
| Ser | Ala | Ile | Val | Asp | Gly | Pro | Pro | Pro | Arg | Leu | Pro | Ser | Asp | Lys | Phe | | |
| | | 595 | | | | 600 | | | | | | 605 | | | | | |
| Ser | Ser | Asp | Ala | Gln | Asp | Phe | Val | Ser | Leu | Cys | Leu | Gln | Lys | Ile | Pro | | |
| | 610 | | | | 615 | | | | | | 620 | | | | | | |
| Glu | Arg | Arg | Pro | Thr | Tyr | Ala | Ala | Leu | Thr | Glu | His | Pro | Trp | Leu | Val | | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | | |
| Lys | Tyr | Arg | Asn | Gln | Asp | Val | His | Met | Ser | Glu | Tyr | Ile | Thr | Glu | Arg | | |
| | | | 645 | | | | | 650 | | | | | | 655 | | | |
| Leu | Glu | Arg | Arg | Asn | Lys | Ile | Leu | Arg | Glu | Arg | Gly | Glu | Asn | Gly | Leu | | |
| | | 660 | | | | | 605 | | | 608 | | | | | | | |
| Ser | Lys | Asn | Val | Pro | Ala | Leu | His | Met | Gly | Gly | Leu | | | | | | |

(2) INFORMATION FOR SEQ ID NO:14:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
 TTTTAYGGNG CNTTYYTYAT HGA

2/13

(2) INFORMATION FOR SEQ ID NO:15:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3636 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
 ATBCTYTCNG GNGCCATKTA

20

(2) INFORMATION FOR SEQ ID NO:16:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: peptide
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 8
Asp Tyr Lys Asp Asp Asp Asp Lys